SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> Novel Polypeptides, cDNA coding these polypeptides and Use thereof

<130> ONF-2975PCT

<141> 1999-05-13

<150> JP 10-131815

<151> 1998-05-14

<160> 19

<170> PatentIn Ver. 2.0

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<211> 344

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Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro
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Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val
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His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp
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Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr
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Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala
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Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr
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Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala
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Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr
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Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
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Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp Tyr
215 220 225
Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val Glu
230 235 240
Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu His
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Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr
265 270 275
Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val Ser
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Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly
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Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu
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Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser
85 90 95

agg gtc cac ctc att gtg caa gta tct ccc aaa att gta gag att tct 555
Arg Val His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser
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Ser Asp Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile
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Lys Ala Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly
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Ile Thr Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp
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180 185 190

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Pro Tyr Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys
195 200 205 210

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Gly Thr Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln
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Trp Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys
230 235 240

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Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly
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His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu
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295 300 305

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<213> Homo sapiens

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Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln
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Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly
65                  70                  75                  80
Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg
                85                  90                  95
Val His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser
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Asp Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala
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165 170 175
Ala Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro
180 185 190
Tyr Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly
195 200 205
Thr Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp
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Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val
225 230 235 240
Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu
245 250 255
His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His
260 265 270
Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val
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atctctccca aagcggttgg ctttgtgagt gaagacgaat acttggaaat tcagggcatc 480

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35 40 45

Leu Glu Gly Asp Lys Gln Leu Ile Arg Glu Thr Ser Thr His Gln Leu
50 55 60

Asn Ser Glu Arg Tyr Val His Thr Phe Lys Asp Leu Ser Asn Phe Ser
65 70 75 80

Gly Ala Ile Asn Val Thr Tyr Arg Tyr Leu Ala Ala Thr Pro Leu Gln
85 90 95

Arg Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys
100 105 110

Gly Asn Tyr Leu Leu Glu Thr Ile Lys Ser Ile Phe Glu Gln Ser Ser
115 120 125

Tyr Glu Glu Leu Lys Glu Ile Ser Val Val Ile His Leu Ala Asp Phe
130 135 140
Asn Ser Ser Trp Arg Asp Ala Met Val Gln Asp Ile Thr Gln Lys Phe
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Ala His His Ile Ile Ala Gly Arg Leu Met Val Ile His Ala Pro Glu
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Glu Tyr Tyr Pro Ile Leu Asp Gly Leu Lys Arg Asn Tyr Asn Asp Pro
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Glu Asp Arg Val Lys Phe Arg Ser Lys Gln Asn Val Asp Tyr Thr Phe
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Asp Asp Val Arg Cys Ser Lys Asn Phe Leu Thr Ala Ile Lys Lys Val
225 230 235 240
Ile Ala Ser Leu Glu Gly Thr Tyr Trp Val Thr Leu Glu Phe Ser Lys
245 250 255
Leu Gly Tyr Ile Gly Lys Leu Tyr His Ser His Asp Leu Pro Arg Leu
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Ala His Phe Leu Leu Met Phe Tyr Gln Glu Met Pro Cys Asp Trp Leu
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Leu Thr His Phe Arg Gly Leu Leu Ala Gln Lys Asn Val Ile Arg Phe
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Lys Pro Ser Leu Phe Gln His Met Gly Tyr Tyr Ser Ser Tyr Lys Gly
305 310 315 320

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325 330 335
Ile Pro Asp Asn Pro Pro Ala Ser Leu Tyr Thr Asn Met Asn Val Phe
340 345 350
Glu Asn Tyr Glu Ala Ser Lys Ala Tyr Ser Ser Val Asp Glu Tyr Phe
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Trp Gly Lys Pro Pro Ser Thr Gly Asp Val Phe Val Ile Val Phe Glu
370 375 380
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385 390 395 400
Arg Gln Asn Asp Ile Leu His His Gly Ala Leu Asp Val Gly Glu Asn
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Val Met Pro Ser Lys Gln Arg Gly Gln Cys Ser Thr Tyr Leu Arg Leu
420 425 430
Gly Glu Phe Lys Asn Gly Asn Phe Glu Met Ser Gly Val Asn Gln Lys
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Ile Pro Phe Asp Ile His Cys Met Arg Ile Tyr Val Thr Lys Thr Gln
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aagtcaattt ttgagcaatc cagctatgaa gagctgaagg aaatttcagt ggtgattcac 420

ctagcagact ttaattcttc ctggcgtgat gccatggtcc aggatattac acagaaattt 480

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1

ttt aaa ttt cat caa atg aaa cat att ttt gaa ata ctt gat aaa atg 164

Phe Lys Phe His Gln Met Lys His Ile Phe Glu Ile Leu Asp Lys Met

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20 25 30

att ttt ctc ctt ttt atg aac ttg tac att gaa gat agc tat gtt ctg 260

Ile Phe Leu Leu Phe Met Asn Leu Tyr Ile Glu Asp Ser Tyr Val Leu

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Glu Gly Asp Lys Gln Leu Ile Arg Glu Thr Ser Thr His Gln Leu Asn

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tca gaa cgc tat gtt cat act ttc aag gat tta tct aat ttc tca gga 356

Ser Glu Arg Tyr Val His Thr Phe Lys Asp Leu Ser Asn Phe Ser Gly

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Ala Ile Asn Val Thr Tyr Arg Tyr Leu Ala Ala Thr Pro Leu Gln Arg

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Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys Gly

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Asn Tyr Leu Leu Glu Thr Ile Lys Ser Ile Phe Glu Gln Ser Ser Tyr

115 120 125

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Glu Glu Leu Lys Glu Ile Ser Val Val Ile His Leu Ala Asp Phe Asn
130 135 140 145

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His His Ile Ile Ala Gly Arg Leu Met Val Ile His Ala Pro Glu Glu
165 170 175

tat tac cca atc cta gat ggc ctt aaa aga aat tac aat gat cca gaa 692
Tyr Tyr Pro Ile Leu Asp Gly Leu Lys Arg Asn Tyr Asn Asp Pro Glu
180 185 190

gat aga gtc aaa ttt cgt tcc aag caa aat gta gat tat act ttt ctg 740
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195 200 205

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Leu Asn Phe Cys Ala Asn Thr Ser Asp Tyr Tyr Val Met Leu Glu Asp
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230 235 240

gca tcc cta gaa gga act tac tgg gta act ctt gaa ttc tct aag ctt 884
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245 250 255

ggc tac att ggt aaa ctc tat cat tct cat gat ctc cca cgt ttg gcc 932

Gly Tyr Ile Gly Lys Leu Tyr His Ser His Asp Leu Pro Arg Leu Ala

260 265 270

cat ttt tta tta atg ttt tat caa gaa atg cct tgt gat tgg cta ttg 980

His Phe Leu Leu Met Phe Tyr Gln Glu Met Pro Cys Asp Trp Leu Leu

275 280 285

act cat ttc cgt ggt ctg ttg gct cag aaa aat gtg atc cgt ttt aaa 1028

Thr His Phe Arg Gly Leu Leu Ala Gln Lys Asn Val Ile Arg Phe Lys

290 295 300 305

cca tct ctc ttt cag cac atg ggc tat tat tca tca tac aaa ggg acg 1076

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gag aat aag ctg aag gat gat gat ttt gaa gag gag tca ttt gac att 1124

Glu Asn Lys Leu Lys Asp Asp Asp Phe Glu Glu Glu Ser Phe Asp Ile

325 330 335

cct gat aac ccc cct gca agt ctg tac acc aac atg aat gtg ttt gaa 1172

Pro Asp Asn Pro Pro Ala Ser Leu Tyr Thr Asn Met Asn Val Phe Glu

340 345 350

aat tat gaa gca agc aag gct tac agt agt gtt gat gag tac ttt tgg 1220

Asn Tyr Glu Ala Ser Lys Ala Tyr Ser Ser Val Asp Glu Tyr Phe Trp

355 360 365

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390 395 400

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405 410 415

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Met Pro Ser Lys Gln Arg Gly Gln Cys Ser Thr Tyr Leu Arg Leu Gly

420 425 430

gaa ttc aaa aat gga aac ttt gaa atg tca ggt gta aat caa aaa att 1460

Glu Phe Lys Asn Gly Asn Phe Glu Met Ser Gly Val Asn Gln Lys Ile

435 440 445

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Pro Phe Asp Ile His Cys Met Arg Ile Tyr Val Thr Lys Thr Gln Lys

450 455 460 465

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Glu Trp Leu Ile Ile Arg Ser Ile Ser Ile Trp Thr Ser

470 475

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tttggaggga aagcaatgga tgggatatgt taaaagaaac attaattaca ttggcagttt 1677

tcatttatac attgttgaca taattttact cttaatacac acttgtattt attttaacgt 1737

ctgaagttga atatcagtct atagctaatg ctactttcat ttatattttt aaatgttctt 1797

agttttaaaa tttcaactga ttgtcgaaag ggtaatatga aagattttaa atgaaaaaaa 1857

tttgttggat gatgattttt gaaaaatagt caccaactgt atatacttcc tcaagaactg 1917

ataattcatt atatcatcag atagctttta ttaagcatct gtgggaatat acagttgggt 1977

ggaatgataa tctggtttat tttttctgta aacttaagtt tccgttgact tctgtacatc 2037

tacaatgaat acctcctcat agaagtggtg tctttacata atttttttgtg taggtgacac 2097

tatggaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 2131

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<211> 335

<212> PRT

<213> Homo sapiens

<400> 9

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Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile
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Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe
35 40 45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser
50 55 60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile
65 70 75 80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe
85 90 95

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu

100 105 110

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe

115 120 125

Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln

130 135 140

Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr

145 150 155 160

Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr

165 170 175

Leu Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys

180 185 190

Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu

195 200 205

Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val

210 215 220

Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser

225 230 235 240

Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr

245 250 255

Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His

260 265 270

Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro

275 280 285

Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr

290 295 300

Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu

305 310 315 320

Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys

325 330 335

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<211> 1005

<212> DNA

<213> Homo sapiens

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ctcatggcgc tgctgcccat cttcttcggc gccctgcgct ccgtacgctg cgcccgcggc 180

aagaatgctt cagacatgcc tgaaacaatc accagccggg atgccgcccg cttccccatc 240

atcgccagct gcacactctt ggggctctac ctctttttca aaatattctc ccaggagtac 300

atcaacctcc tgctgtccat gtatttcttc gtgctgggaa tcctggccct gtcccacacc 360

atcagccccc tcatgaataa gtttttttcca gccagctttc caaatcgaca gtaccagctg 420

ctcttcacac agggttctgg ggaaaacaag gaagagatca tcaattatga atttgacacc 480

aaggacctgg tgtgcctggg cctgagcagc atcgttggcg tctggtacct gctgaggaag 540

gtatttggca ccaatgtgat ggtgacagtg gccaagtcct tcgaggcacc aataaaattg 600

gtgtttcccc aggatctgct ggagaaaggc ctcgaagcaa acaactttgc catgctggga 660

cttggagatg tcgtcattcc agggatcttc attgccttgc tgctgcgctt tgacatcagc 720

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atgttcagtt atgaggagtc aaatcctaag gatccagcgg cagtgacaga atccaaagag 960

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<210> 11

<211> 1486

<212> DNA

<213> Homo sapiens

<220>

<223> Clone OA004b derived from T98G cell

<220>

<221> CDS

<222> (117)..(1121)

<400> 11

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Met

gac tcg gcc ctc agc gat ccg cat aac ggc agt gcc gag gca ggc ggc 167
Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly
5 10 15

ccc acc aac agc act acg cgg ccg cct tcc acg ccc gag ggc atc gcg 215
Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala
20 25 30

ctg gcc tac ggc agc ctc ctg ctc atg gcg ctg ctg ccc atc ttc ttc 263
Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe Phe
35 40 45

ggc gcc ctg cgc tcc gta cgc tgc gcc cgc ggc aag aat gct tca gac 311
Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp
50 55 60 65

atg cct gaa aca atc acc agc cgg gat gcc gcc cgc ttc ccc atc atc 359
Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile
70 75 80

gcc agc tgc aca ctc ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc 407
Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser
85 90 95

cag gag tac atc aac ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga 455
Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly
100 105 110

atc ctg gcc ctg tcc cac acc atc agc ccc ttc atg aat aag ttt ttt 503
Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe

115 120 125

cca gcc agc ttt cca aat cga cag tac cag ctg ctc ttc aca cag ggt 551
Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly
130 135 140 145

tct ggg gaa aac aag gaa gag atc atc aat tat gaa ttt gac acc aag 599
Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys
150 155 160

gac ctg gtg tgc ctg ggc ctg agc agc atc gtt ggc gtc tgg tac ctg 647
Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu
165 170 175

ctg agg aag gta ttt ggc acc aat gtg atg gtg aca gtg gcc aag tcc 695
Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys Ser
180 185 190

ttc gag gca cca ata aaa ttg gtg ttt ccc cag gat ctg ctg gag aaa 743
Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys
195 200 205

ggc ctc gaa gca aac aac ttt gcc atg ctg gga ctt gga gat gtc gtc 791
Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val
210 215 220 225

att cca ggg atc ttc att gcc ttg ctg ctg cgc ttt gac atc agc ttg 839
Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu
230 235 240

aag aag aat acc cac acc tac ttc tac acc agc ttt gca gcc tac atc 887
Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile

245 250 255

ttc ggc ctg ggc ctt acc atc ttc atc atg cac atc ttc aag cat gct 935
Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His Ala
260 265 270

cag cct gcc ctc cta tac ctg gtc ccc gcc tgc atc ggt ttt cct gtc 983
Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val
275 280 285

ctg gtg gcg ctg gcc aag gga gaa gtg aca gag atg ttc agt tat gag 1031
Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu
290 295 300 305

gag tca aat cct aag gat cca gcg gca gtg aca gaa tcc aaa gag gga 1079
Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly
310 315 320

aca gag gca tca gca tcg aag ggg ctg gag aag aaa gag aaa 1121
Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys
325 330 335

tgatgcggct ggtgcccgag cctctcaggg ccagaccaga cagatggggg ctgggcccac 1181

acaggcgtgc accggtagag ggcacaggag gccaagggca gctccaggac agggcagggg 1241

gcagcaggat acctccagcc aggcctctgt ggcctctgtt tccttctccc tttcttggcc 1301

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<210> 12

<211> 360

<212> PRT

<213> Homo sapiens

<400> 12

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Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile Asn Val Arg
  1               5                  10                  15

Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn Ser Asn Asn
            20                  25                  30

Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn Arg Pro Val
        35                  40                  45

Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys Ser Phe Leu
    50                  55                  60

Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp Leu Gln Ala
65                  70                  75                  80

Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu Gly Gln Glu
                85                  90                  95

Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser Leu Glu Ala
            100                 105                 110

Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro Asp Leu Ala
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115 120 125

Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro Met Tyr Val

130 135 140

Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu

145 150 155 160

Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile

165 170 175

Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile

180 185 190

Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn

195 200 205

Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys

210 215 220

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro Asn

225 230 235 240

Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp Asn Pro

245 250 255

Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu Val Glu Val

260 265 270

Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe Lys Cys Phe

275 280 285

Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr

290 295 300

Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys Val Ala Arg

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Leu Ala Ala Lys Ala Leu Ala Ser Val Ser Gly Thr Glu Tyr Gln Val

325 330 335

Gly Pro Thr Cys Thr Thr Val Leu

340

<210> 13

<211> 1080

<212> DNA

<213> Homo sapiens

<400> 13

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aatcggcctg tggatgtcct ggtcccatct gtcagtctgc aggcatttaa atccttcctg 240

agatcccagg gcttagagta cgcagtgaca attgaggacc tgcaggccct tttagacaat 300

gaagatgatg aaatgcaaca caatgaaggg caagaacgga gcagtaataa cttcaactac 360

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cctgacctgg cgaggagggt gaagattgga cattcgtttg aaaaccggcc gatgtatgta 480

ctgaagttca gcactgggaa aggcgtgagg cggccggccg tttggctgaa tgcaggcatc 540

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gattaccaga gggatccagc tatcacctcc atcttggaga aaatggatat tttcttgttg 660

cctgtggcca atcctgatgg atatgtgtat actcaaactc aaaaccgatt atggaggaag 720

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tcagtcaaaa aggccccaga tgccgaggaa ctcgacaagg tggcgaggct tgcggccaaa 1020

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<210> 14

<211> 3156

<212> DNA

<213> Homo sapiens

<220>

<223> Clone OAF075b derived from human bone marrow stroma cell HAS303

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<221> CDS

<222> (11)..(1090)

<220>

<221> sig_peptide

<222> (11)..(58)

<220>

<221> mat_peptide

<222> (59)..(1090)

<400> 14

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          Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser
              -15                 -10                 -5

agc atc tgt ggc caa gaa aaa ttt ttt ggg gac caa gtt ttt agg att    97
Ser Ile Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile
        -1  1               5                  10

aat gtc aga aat gga gac gag atc agc aaa ttg agt caa cta gtg aat   145
Asn Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
    15                  20                  25

tca aac aac ttg aag ctc aat ttc tgg aaa tct ccc tcc tcc ttc aat   193
Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn
30                  35                  40                  45

cgg cct gtg gat gtc ctg gtc cca tct gtc agt ctg cag gca ttt aaa   241
Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys
                50                  55                  60

tcc ttc ctg aga tcc cag ggc tta gag tac gca gtg aca att gag gac   289
Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp
            65                  70                  75
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ctg cag gcc ctt tta gac aat gaa gat gat gaa atg caa cac aat gaa 337
Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu
80 85 90

ggg caa gaa cgg agc agt aat aac ttc aac tac ggg gct tac cat tcc 385
Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser
95 100 105

ctg gaa gct att tac cac gag atg gac aac att gcc gca gac ttt cct 433
Leu Glu Ala Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro
110 115 120 125

gac ctg gcg agg agg gtg aag att gga cat tcg ttt gaa aac cgg ccg 481
Asp Leu Ala Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro
130 135 140

atg tat gta ctg aag ttc agc act ggg aaa ggc gtg agg cgg ccg gcc 529
Met Tyr Val Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala
145 150 155

gtt tgg ctg aat gca ggc atc cat tcc cga gag tgg atc tcc cag gcc 577
Val Trp Leu Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala
160 165 170

act gca atc tgg acg gca agg aag att gta tct gat tac cag agg gat 625
Thr Ala Ile Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp
175 180 185

cca gct atc acc tcc atc ttg gag aaa atg gat att ttc ttg ttg cct 673
Pro Ala Ile Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro
190 195 200 205

gtg gcc aat cct gat gga tat gtg tat act caa act caa aac cga tta 721
Val Ala Asn Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu
210 215 220

tgg agg aag acg cgg tcc cga aat cct gga agc tcc tgc att ggt gct 769
Trp Arg Lys Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala
225 230 235

gac cca aat aga agc tgg aac gct agt ttt gca gga aag gga gcc agc 817
Asp Pro Asn Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser
240 245 250

gac aac cct tgc tcc gaa gtg tac cat gga ccc cac gcc aat tcg gaa 865
Asp Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu
255 260 265

gtg gag gtg aaa tca gtg gta gat ttc atc caa aaa cat ggg aat ttc 913
Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe
270 275 280 285

aag tgc ttc atc gac ctg cac agc tac tcg cag ctg ctg atg tat cca 961
Lys Cys Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro
290 295 300

tat ggg tac tca gtc aaa aag gcc cca gat gcc gag gaa ctc gac aag 1009
Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys
305 310 315

gtg gcg agg ctt gcg gcc aaa gct ctg gct tct gtg tcg ggc act gag 1057
Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val Ser Gly Thr Glu
320 325 330

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Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Leu
335 340

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ccatttttg ttgttgttat tgtttttaaa gagtaggtag actttcagca gggacccaaa 3090

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aaaaaa 3156

<210> 15

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 15

cgattgaatt ctagacctgc ctcgagnnnn nnnnn

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer OC001-F1

<400> 16

gtccttcagc aaaacagtgg atttaaa 27

<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer OM237-F1

<400> 17

ccagaaagca cagccctgat tctgcgt 27

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer OA004-F1

<220>

<221> modified base

<222> 1

<223> biotin conjugated base

<400> 18

atgcacatct tcaagcatgc tcag 24

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer OAF075-F1

<400> 19

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